

SCORE Search Results Details for Application  
10796719 and Search Result  
20070322\_090632\_us-10-796-719a-31.rag.

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:36:07 ; Search time 218 Seconds
              (without alignments)
              31.425 Million cell updates/sec
```

```
Title:      US-10-796-719A-31
Perfect score: 101
Sequence:   1 CCEYCCNPACTGCGY 14
```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_200701:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:37:42 ; Search time 346 Seconds
              (without alignments)
              43.381 Million cell updates/sec
```

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCGY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      UniProt_8.4:*
1:  uniprot_sprot:*
2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	93	92.1	61	2	Q6VEG7_ECOLI	Q6veg7 escherichia
2	93	92.1	61	2	Q6VEG8_ECOLI	Q6veg8 escherichia
3	93	92.1	72	1	HST2 ECOLI	Q47185 escherichia

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:47:23 ; Search time 51 Seconds
              (without alignments)
              24.028 Million cell updates/sec
```

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCGY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
--------	------------

# SCORE Search Results Details for Application 10796719 and Search Result 20070322\_090649\_us-10-796-719a-31.rapbm.

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GenCore version 6.2  
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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:48:07 ; Search time 186 Seconds
              (without alignments)
              34.866 Million cell updates/sec
```

```
Title:      US-10-796-719A-31
Perfect score: 101
Sequence:   1 CCEYCCNPACTGCGY 14
```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database :      Published_Applications_AA_Main:*
1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Match	Length	DB	ID	Description

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 00:49:03 ; Search time 90 Seconds
              (without alignments)
              31.666 Million cell updates/sec
```

```
Title:      US-10-796-719A-31
Perfect score: 101
Sequence:   1 CCEYCCNPACTGCY 14
```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_AA_New:*
1:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

o/c

SCORE Search Results Details for Application  
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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 17:56:43 ; Search time 218 Seconds
              (without alignments)
              38.159 Million cell updates/sec
```

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      A_Geneseq_200701:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: March 23, 2007, 17:59:13 ; Search time 344 Seconds  
(without alignments)  
52.983 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPACFGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	112	100.0	17	2 Q9R581_VIBCH	Q9r581 vibrio chol
2	112	100.0	18	2 Q9R580_VIBCH	Q9r580 vibrio chol
3	112	100.0	19	2 Q9R579_VIBCH	Q9r579 vibrio chol

# SCORE Search Results Details for Application 10796719 and Search Result 20070323\_110727\_us-10-796-719a-14.rpr.

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GenCore version 6.2

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:02:53 ; Search time 39 Seconds
              (without alignments)
              41.941 Million cell updates/sec
```

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      PIR_80:*
            1:  pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID		Description
1	112	100.0	17	2	A54534		heat-stable enterotoxin



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GenCore version 6.2

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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:09:29 ; Search time 52 Seconds
              (without alignments)
              28.616 Million cell updates/sec
```

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	% Query
--------	------------

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OM protein - protein search, using sw model

Run on: March 23, 2007, 18:09:38 ; Search time 184 Seconds  
(without alignments)  
42.797 Million cell updates/sec

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPAFCGCLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	%				Description
No.	Score	Match Length	DB	ID		

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GenCore version 6.2  
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OM protein - protein search, using sw model

```
Run on:      March 23, 2007, 18:10:53 ; Search time 89 Seconds
              (without alignments)
              38.883 Million cell updates/sec
```

Title: US-10-796-719A-14  
Perfect score: 112  
Sequence: 1 IDCCEICCNPAFCGLN 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      Published_Applications_AA_New:*
1:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8:   /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore version 6.2

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OM protein - protein search, using sw model

```
Run on:      March 26, 2007, 11:50:46 ; Search time 218 Seconds
              (without alignments)
              31.425 Million cell updates/sec
```

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCGY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database :      A_Geneseq_200701:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.







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GenCore version 6.2  
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OM protein - protein search, using sw model

Run on: March 26, 2007, 12:03:06 ; Search time 185 Seconds  
(without alignments)  
35.054 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	%				
No.	Score	Match Length	DB	ID	Description	



# SCORE Search Results Details for Application 10796719 and Search Result 20070326\_091535\_us-10-796-719a-31.rapbn.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10796719 and Search Result 20070326\_091535\_us-10-796-719a-31.rapbn.

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GenCore version 6.2  
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OM protein - protein search, using sw model

Run on: March 26, 2007, 12:04:21 ; Search time 89 Seconds  
(without alignments)  
32.021 Million cell updates/sec

Title: US-10-796-719A-31  
Perfect score: 101  
Sequence: 1 CCEYCCNPACTGCY 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 932539 seqs, 203564912 residues

Total number of hits satisfying chosen parameters: 932539

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%